



#5

NOVTRAN cDNA sequence:

atgcagtggctcctgtctggcctgtaccctcctcagggctcctcccacatgtcctgtctctcctgagagaccctgtgcctgtgccacagggaccaagctcttc
cactcctgtatcacctcaacgaacccatgcgcctccttctcctggaggttgctgttgaaagctgcaggcatcacccctggactgtagggctctgagcaccogcc
ctgtccatataccatccctgcatgcctctcogttcacccactccttcaacagaccatccctgctcctctcaacaggcccgctctgctggggaacca
cggacagaggccttccatccccaggcctgaaggccagagtgggtggaccatcctcgccgaagccggcctcaattctcaaggccatgccgtggagc
cagtgccatctggaccctctgggtcaagcaagggtgtgtgctaataaaaggcaggccctcgaggatgccaaaggcccggaatgccagtggaaccg
tgaaaaaccttctgtgacaaacctgcagtgccttctctgtctccagctgctctccagctctccatgcataaggtggaaacagagcaggagcgcagtaatg
cggaatttgacttgcaagtcgggccgctcgggattacaattcaaggtgctgctgaaactcgggcagatcccagctgcaaaaggcagttccttctcga
gctgcagaacgtgtctggaggggttggtcagcccgaggtcccaggaaccactgcaaggtggggcgggccctcagagcccttcccagagctggg
ggctggtagcccccttggcttggagaaggtcagtaccaaccattcccagggccgactgcggaagggtgtggaactggccccctgtgtctcctggt
gaccagtgtccactgtgcactctcccagggcagccgaacctggcacacactgggtgttccctaaatagccatggagggtattgtggcatggagagctgtc
gattccagaaacctcctggacatagggtcgggagctcatctgcagaagctgcctga (SEQ ID NO: 1)

Fig. 1A

NOVTRAN Protein Sequence:

MQWSCLACTLLRVLPHVLSLLRDPVPVPTGTKLFHSCITSTNPCASFLEVAVEAAGITPW
TVGSEHPPCPYPSSLHASPF'TDSFNRPSPAPLNRPRSAGEPRTEAFPSPLKARVGGTILAE
AGLNSQGHAVEPVPSGPGSSSKGCVLIKGRPSRMPKARECPVDRENLLL TNPAVPSLLQL
LSSSPCIKVETEQRSENAEFDLQSRARDYNSRLLLKLQIIPAAKGSSFLELQNVSGGVG
SARGPRNHCKVAGPQSPFPELGAGSPPLALEKVSTQPI PQARLRKGVDPWPVSPGDQC
PLCTLPGPQPNLAHTGCSLNSHGGYCGMESCRFQKPPGHRAGSSSAEAA (SEQ ID NO: 2)

Fig. 1B

05730617-070904

BlastN for NOVTRAN:
gb:GENBANK-ID:H55724|acc:H55724 CHR220663 Chromosome 22 exon Homo sapiens
genomic clone C22_916 5', mRNA sequence - Homo sapiens, 171 bp.

Minus Strand HSPs:

Score = 585 (87.8 bits), Expect = 1.0e-19, P = 1.0e-19
Identities = 117/117 (100%), Positives = 117/117 (100%), Strand = Minus /
Plus

Query: 735 ACCTCGGGCTGAGCCAACCCCTCCAGACAGTTCTGCAGCTCGAGGAAGGAACTGCCCTT 676

Sbjct: 18 ACCTCGGGCTGAGCCAACCCCTCCAGACAGTTCTGCAGCTCGAGGAAGGAACTGCCCTT 77

Query: 675 TGCAGCTGGGATCTGCCCGAGTTTCAGCAGCAGCCTTGAATTGTAATCCCGAGCGGC 619 (SEQ ID NO: 19)

Sbjct: 78 TGCAGCTGGGATCTGCCCGAGTTTCAGCAGCAGCCTTGAATTGTAATCCCGAGCGGC 134 (SEQ ID NO: 20)

Fig. 2A

T06040-4902-50

BlastX for NOVTRAN:

NoHits:

ptnr:SWISSPROT-ACC:P22357 ANHER-SPECIFIC PROTEIN SF18...	-3	102	0.0093	1
ptnr:SPTREMBL-ACC:Q26876 PROTECTIVE RECOMBINANT ANTIGE...	-3	87	0.018	1
ptnr:TREMBLNEW-ACC:AAD41775 PRO-ALPHA-2(I) COLLAGEN - ...	-3	86	0.061	2
ptnr:PIR-ID:S46272 anther-specific protein - common su...	-3	94	0.073	1
ptnr:SPTREMBL-ACC:Q26874 PROTECTIVE RECOMBINANT ANTIGE...	-3	78	0.16	1
ptnr:SPTREMBL-ACC:Q92029 ALPHA-1 COLLAGEN TYPE III - G...	-3	86	0.19	3
ptnr:SWISSPROT-ACC:P46804 SPIDROIN 2 (DRAGLINE SILK FI...	-3	101	0.24	1
ptnr:SPTREMBL-ACC:Q57808 103AA LONG HYPOTHETICAL PROTE...	+2	76	0.25	1
ptnr:SWISSNEW-ACC:P41484 PROLINE-RICH ANTIGEN (36 KD A...	-3	95	0.26	1

CuraBLASTX Analysis of AC007663_A

PUBLIC DATABASE

Query= AC007663 A Cura 109 transmembrane protein
(1047 letters)

Database: /opt/database/public/blast/protnr
577,633 sequences; 178,813,065 total letters.

		Smallest		Sum	
			Reading	High	Probability
Sequences producing High-scoring Segment Pairs:		Frame	Score	P(N)	N
ptnr:SWISSPROT-ACC:P22357 ANHER-SPECIFIC PROTEIN SF18	-3	102	0.015	1	
ptnr:pir-id:S12246 anther-specific protein SF18 precur	-3	102	0.015	1	

PATENT DATABASE

CuraBLASTX Analysis of AC007663 A

Query= AC007663 A Cura 109 transmembrane protein
(1047 letters) of query sequence in all 6 reading frames

Database: /opt/database/licensed/blast/geneseq aa
349,121 sequences; 51,277,408 total letters.

		Smallest		Sum	
			Reading	High	Probability
Sequences producing High-scoring Segment Pairs:		Frame	Score	P(N)	N
patp:R28916 Type III procollagen (prior art) - Homo sa...	+1	81	0.059	3	
patp:W03454 Mutant mouse c-AKT non-translation region ...	+1	81	0.075	1	
patp:G04146 Arabidopsis thaliana protein fragment SEQ ...	-3	80	0.095	1	

Fig. 2B

T05070-7906260

NOVNEUR cDNA sequence:

Regions 135319 to 135129 (1-190bp) and 134487 to 134314 (191 to 364bp) of the genomic clone (in - frame). Further extended using ESTs AI739078, AI767488, and AI796217.

AGCGCGCCCGAACGAAGCCGCGGCCCCGGGCACAGCATGGCCCGCGGCGGGAGGGCGCTCGGATGTTCGGC
AGCCTCCTGCACTTCGCCCTGCTCGCTGCCGGCGTCGTCCCGCTCAGCTGGGATCTCCCGGAGCCCCGCA
GCCGAGCCAGCAAGATCCGAGTGCACTCGCGAGGCAAGCTCTGGGCCATCGGTCACTTCATGGGCAAGAA
GAGTCTGGAGCCTTCCAGCCCATCCCCATTGGGGACAGCTCCCCACACCTCCCTGAGGGACCAGCGACTG
CAGCTGAGTCATGATCTGCTCGGAATCCTCCTGCTAAAGAAGGCTCTGGGCGTGAGCCTCAGCCGCCCCG
CACCCCAAATCCAGTACAGGAGGCTGCTGGTACAAATACTGCAGAAATGACACCAATAATGGGGCAGACA
CAACAGCGTGGCTTAGATTGTGCCCACCCAGGGAAGGTGCTGAATGGGACCCTGTTGATGGCCCCATCTG
GATGTAAATCCTGAGCTCAAATCTCTGTTACTCCATTACTGTGATTTCTGGCTGGGTCACCAGAAATATC
GCTGATGCAGACACAGATTATGTTTCCTGCTGTATTTCTGCTTCCCTGTTGAATTGGTGAATAAACCTT
GCTCTATACATACAAA (SEQ ID NO: 3)

Fig. 3A

NOVNEUR Protein sequence:

MFGSLLHFALLAAGVVPLSWDLPEPRSRASKIRVHSRGKLWAIGHFMGKKSLEPSSPSPLGTAPHTSLRDQRLQLSH
DLGILLKKALGVSLSRPAPQIQYRLLVQILQK (SEQ ID NO: 4)

Fig. 3B

BlastN for NOVNEUR:

gb:GENBANK-ID:HUMNKB|acc:M21551 Human neuromedin B mRNA, complete cds -
Homo sapiens, 640 bp (RNA).

Top Previous Match Next Match

Length = 640

Plus Strand HSPs:

Score = 3055 (458.4 bits), Expect = 9.1e-132, P = 9.1e-132

Identities = 629/639 (98%), Positives = 629/639 (98%), Strand = Plus / Plus

Query 2 GCGCGCCCGAACGAAGCCGCGGCGCGGCGACAGC-ATGGCCCG-CGG-CGGGAGGGCGCT 58
GCGCGCCCGAACGAAGCCGCGGCGCGGCGACAGC ATGGCCCG CGG CGGG GGGCGCT
Sbjct: 2 GCGCGCCCGAACGAAGCCGCGGCGCGGCGACAGC-ATGGCCCGCGGCGGGG-GGGCGCT 60

Query: 59 CGGATGTTGGGAGCCCTCTGCACTTCGCGCTGCGTGGCGGCGTGGTCCCGCTCAGC 118
CGGATGTTGGGAGCCCTCTGCTC CTTCGCGCTGCTGCTGCGCGGCTGG CCGCTCAGC
Sbjct: 61 CGGATGTTGGGAGCCCTCTGCTCTTCGCGCTGCTGCTGCGCGGCTGGCGGCTCAGC 120

Query: 119 TGGGATCTCCCGAGCCCCGAGCCGAGCCAGCAAGATCCGAGTGCACTCGCGAGGCAAG 178
TGGGATCTCCCGAGCCCCGAGCCGAGCCAGCAAGATCCGAGTGCACTCGCGAGGCAA
Sbjct: 121 TGGGATCTCCCGAGCCCCGAGCCGAGCCAGCAAGATCCGAGTGCACTCGCGAGGCAAC 180

Query: 179 CTCTGGGCCATCGGTCACTTCATGGGCAAGAAGAGTCTGGAGCCCTCCAGCCCATCCCCA 238
CTCTGGGCCA CGGTCACTTCATGGGCAAGAAGAGTCTGGAGCCCTCCAGCCCATCCC A
Sbjct: 181 CTCTGGGCCACCGGTCACTTCATGGGCAAGAAGAGTCTGGAGCCCTCCAGCCCATCCC-A 239

Query: 239 TTGGGGACAGCTCCCCACACCTCCC-TGAGGGACCAGCGACTGCAGCTGAGTCATGATCT 297
TTGGGGACAGCTCCCCACACCTCCC TGAGGGACCAGCGACTGCAGCTGAGTCATGATCT
Sbjct: 240 TTGGGGACAGCTCCCCACACCTCCCCTGAGGGACCAGCGACTGCAGCTGAGTCATGATCT 299

Query: 298 GCTCGGAATCCTCTGCTAAAGAAGGCTCTGGGCGTGAGCCTCAGCCGCCCCGACCCCCA 357
GCTCGGAATCCTCTGCTAAAGAAGGCTCTGGGCGTGAGCCTCAGCCGCCCCGACCCCCA
Sbjct: 300 GCTCGGAATCCTCTGCTAAAGAAGGCTCTGGGCGTGAGCCTCAGCCGCCCCGACCCCCA 359

Query: 358 AATCCAGTACAGGAGGCTGCTGGTACAAATACTGCAGAAATGACACCAATAAT-GGGGCA 416
AATCCAGTACAGGAGGCTGCTGGTACAAATACTGCAGAAATGACACCAATAAT GGGGCA
Sbjct: 360 AATCCAGTACAGGAGGCTGCTGGTACAAATACTGCAGAAATGACACCAATAATAGGGGCA 419

Query: 417 GACACAACAGCGTGGCTTAGATTGTGCCACCCAGGGAAGTGCTGAATGGGACCCGTGT 476
GACACAACAGCGTGGCTTAGATTGTGCCACCCAGGGAAGTGCTGAATGGGACCCGTGT
Sbjct: 420 GACACAACAGCGTGGCTTAGATTGTGCCACCCAGGGAAGTGCTGAATGGGACCCGTGT 479

Query: 477 GATGGCCCCATCTGGATGTAATCCTGAGCTCAAATCTCTGTTACTCCATTACTGTGATT 536
GATGGCCCCATCTGGATGTAATCCTGAGCTCAAATCTCTGTTACTCCATTACTGTGATT
Sbjct: 480 GATGGCCCCATCTGGATGTAATCCTGAGCTCAAATCTCTGTTACTCCATTACTGTGATT 539

Query: 537 TCTGGCTGGGTACCCAGAAATATCGCTGATGCAGACACAGATTATGTTCTGCTGTATTT 596
TCTGGCTGGGTACCCAGAAATATCGCTGATGCAGACACAGATTATGTTCTGCTGTATTT
Sbjct: 540 TCTGGCTGGGTACCCAGAAATATCGCTGATGCAGACACAGATTATGTTCTGCTGTATTT 599

Query: 597 CCTGCTTCCTGTTGAATTGGTGAATAAAACCTTGCTCTAT 637 (SEQ ID NO: 21)
CCTGCTTCCTGTTGAATTGGTGAATAAAACCTTGCTCT T (SEQ ID NO: 22)
Sbjct: 600 CCTGCTTCCTGTTGAATTGGTGAATAAAACCTTGCTCTTT 640 (SEQ ID NO: 23)

Fig. 4A

BlastX for NOVNEUR:

ptnr:SWISSPROT-ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN
B] - Homo sapiens (Human), 121 aa.

Top Previous Match Next Match
Length = 121

Plus Strand HSPs:

Score = 513 (180.6 bits), Expect = 1.9e-48, P = 1.9e-48
Identities = 105/118 (88%), Positives = 105/118 (88%), Frame = +2

Query: 44 RREGARMFGSLLHFALLAAGVPLSWDLPEPRSRASKIRVHSRGKLWAIGHFMGKKSLEP 223
R GARMFGSLL FALLAAGV PLSWDLPEPRSRASKIRVHSRG LWA GHFMGKKSLEP
Sbjct: 4 RAGGARMFGSLLLALLAAGVAPLSWDLPEPRSRASKIRVHSRGNLWATGHFMGKKSLEP 63

Query: 224 SSPSPGLTAPHTSLRDQRLQLSHDLLGILLKKALGVSLSRPAPQIQYRRLVQILQK 397 (SEQ ID NO: 24)
SSPS G P LRDQRLQLSHDLLGILLKKALGVSLSRPAPQIQYRRLVQILQK (SEQ ID NO: 25)
Sbjct: 64 SSPSHWGQLPTPLRDQRLQLSHDLLGILLKKALGVSLSRPAPQIQYRRLVQILQK 121 (SEQ ID NO: 26)

Fig. 4B

ClustalW for NOVNEUR:

Based on this alignment, black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties); greyed amino acid residues can be mutated to a residue with comparable steric and/or chemical properties without altering protein structure or function (e.g., L to V, I, or M); non-highlighted amino acid residues can potentially be mutated to a much broader extent without altering structure or function.

Sequences used:

- 1) A37178 (neuromedin B precursor - rat): Locus A37178, accession A37178, PID - g1 12182
- 2) NEUB_HUMAN (NEUROMEDIN B-32 PRECURSOR): Locus - NEUB_HUMAN, accession - P08949, PID - g1346684

Neuromedin_New_REVCOMP -----MFGSLLHFALLAAGVPLSWDLPEPRSRASKIRVHSRGKLWAIGHFMGKKS
A37178 MTRQAGSTWLLRGHLLFALFVSCITEPSWDLPEPRSRASKIRVHSRGNLWATGHFMGKKS
NEUB_HUMAN MARRAGGARMFGSLLLALLAAGVAPLSWDLPEPRSRASKIRVHSRGNLWATGHFMGKKS

Neuromedin_New_REVCOMP LEPSSPSPLGTAPHTSLRDQRLQLSHDLLGILLKKALGVSLSRPAPQIQYRRLVQILQ
A37178 LEPSSLSLVGTAPPTITQRLQLSHDLLGILLKKALGVSLSRPAPPTIQYRRLVQILQ---
NEUB_HUMAN LEPSSPSHWGQLPTPLRDQRLQLSHDLLGILLKKALGVSLSRPAPQIQYRRLVQILQ

Neuromedin_New_REVCOMP K (SEQ ID NO: 27)
A37178 - (SEQ ID NO: 28)
NEUB_HUMAN K (SEQ ID NO: 29)

Fig. 5

NOVGON cDNA sequence:

1
ATGAAGCTGGCATTCTCTTCTTGGCCCCATGGCCCTCCTCCTTCTGGCTGGCTATGGCTGTGTCCTGGTGCCCTCCAG
81
TGGGAACCTGGGCACCTTTGTGGGCTGTGCCGTGAGGGAGTTTACTTTCTGGCCAAGAAGCCAGGCTGCAGGGCCCTTC
161
GGATCACCACGGATGCCCTGTGGGGTGGCTGTGAGACCTGGGAGAAACCCATTCTGGAACCCCTATATTGAAGCCCAT
241
CATCGAGTCTGTACCTACAACGAGACCAACAGGTGACTGTCAAGCTGCCCAACTGTGCCCCGGGAGTCGACCCCTTCTA
321
CACCTATCCCGTGGCCATCCGCTGTGACTGCGGAGCCTGCTCCACTGCCACCAAGGAGCTGAGGTTGATGCCAGGGGAAG
401
CTGCTGTGGCACTGGGCTTCTGGTGTGAGGTAGGAGACAGGATCTAGGACAACAGGACACAGGTGGCGACATGCAGCT
481
CTAAGAGACAAGGTGAGTCTCCTGAAGGCAGTAGATGGTTGGAATGGGCTGCTTGGGGACCCAGCGAGCTCCAGGGCCT
561
TTCTGCTTCTTCTGTACCCCTGTATTTCCCTTGGCTTTCCAAATTGACTCAGCTTCTGGTAAAGTTGGAACTTTTCCA
641
GCAACACAGACCTTCATCTTCTCCAGTGCAGAGATTACATTAGGAGGAACATGA (SEQ ID NO: 5)

Fig. 6A

NOVGON Protein Sequence:

MKLAFLFLGPMALLLLAGYGCVLGASSGNLRTFVGCAVREFTFLAKKPGCRGLRITTD
CWGRCEIWEKPILEPPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTPVAIRCDG
ACSTATTELRLMPGEAAVALGFWCQRRRQGSRTTGTWRHAAVRDKVSLKAVDGN
NGLLGDPASSQGLSASSCTPVFPLAFQIDSASGKVGNFSSKQTFIFSSAETLGGT* (SEQ ID NO: 6)

Fig. 6B

BlastN for NOVGON:

AF146151 *Salmo salar* gonadotropin II beta subunit mRNA,
partial cds - *Salmo salar*, 266 bp (RNA).

Top Previous Match Next Match
Length = 266

Plus Strand_HSPs:

Score = 208 (31.2 bits), Expect = 0.043, P = 0.042

Identities = 124/205 (60%), Positives = 124/205 (60%), Strand = Plus / Plus

Query: 177 CTGCTGGGGTCGCTGTGAGACCTGGGAGAAACCCATTTCGGAACCCCTATATGAAGC 236
CTGC G GG C CTG G ACC GGAG CC TT T AA CCC AT TT A C
Sbjct: 34 CTGCAGTGGCCACTGCGTCACCAAGGAG---CCGGTTTTC-AAGAGCCC-ATTTTCCACC 88

Query: 237 CCAT-C-ATCGAGTCTGTACCTACAACGA-GACCAAACAGGTGACTGTCAAGCTGCCCAA 293
T C A C GT TG ACCTAC GA G CC A G AC TC CT CC A
Sbjct: 89 GTGTACCAGCATGTGTGCACCTACCGGGACGTCCGCT-ATGAAACGATCCGCCTACCTGA 147

Query: 294 CTGTGCCCCGGGAGTCGACCC-CTTCTACACCTATCCCGTGGCCATCCGCTGTGACTGCG 352
CTGT CCCC G GT GACC C T T CACCTA CC GTGGC T GCTGTGACTGC
Sbjct: 148 CTGTCCCCCTTGGGTGGACCATCATGT-CACCTACCTGTGGCTCTGAGCTGTGACTGCA 206

Query: 353 GAGCCTGCTCCACTGCCACCACGGAGCTG 381 (SEQ ID NO: 30)
G CTG CA G CAC C GA CTG (SEQ ID NO: 31)
Sbjct: 207 GCCTCTGTAAACATGGACACTTCTGA-CTG 234 (SEQ ID NO: 32)

Fig. 7A

BlastX for NOVGON:

P01235 GONADOTROPIN BETA CHAIN PRECURSOR - *Cyprinus carpio* (Common carp), 144 aa.

Score = 203 (71.5 bits), Expect = 2.3e-16, P = 2.3e-16
Identities = 37/85 (43%), Positives = 52/85 (61%)
Query: 42 TFLAKKPGC-RGLRITTDACWGRCETWEKPILEPPYIEAHRVCTYNETKQVTVKLPNCA 100
T +K GC + L + T C G C T E P+ + P+ + VCTY + + TV+LP+C
Sbjct: 39 TVAVEKEGCPKCLVLQTTICSGHCLTKE-PVYKSPFSTVYQHVCTYRDVRYETVRLPDCP 97

Query: 101 PGVDPFYTYTPVAIRCDCGACSTATTE 126 (SEQ ID NO: 33)
PGVDP TYPVA+ CDC C+ T++ (SEQ ID NO: 34)
Sbjct: 98 PGVDPHITYPVALSCDCSLCTMDTSD 123 (SEQ ID NO: 35)

>ptnr:SWISSNEW-ACC:Q9YGH2 GONADOTROPIN BETA-II CHAIN PRECURSOR (GTH-II-BETA)
- *Clupea pallasii* (Pacific herring), 149 aa.
Plus Strand HSPs:

Score = 206 (72.5 bits), Expect = 1.0e-15, P = 1.0e-15
Identities = 47/117 (40%), Positives = 63/117 (53%), Frame = +1
Query: 28 PMALLLLAGYGCVLG--ASSGNLRTFVGCAVREFTFLAKKPGC-RGLRITTDACWGRCET 198
P +LL CVL A NL+ C + T +K GC R L T C G C T
Sbjct: 5 PECTILLLLCMCVLAVPAQCFLNP---CVLVNETVSVEKEGCPRLVFRITICSGHCPT 61

Query: 199 WEKPILEPPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYTPVAIRCDCGACSTATTE 378 (SEQ ID NO: 36)
E P+ + P+ + VCTY + T++LP+CA GVDP TYPVA+ C+C CS T++ (SEQ ID NO: 37)
Sbjct: 62 KE-PVYKSPFSVNVQHVCTYGNFRYETIRLPDCADGVDPVLTYPVALSCECSLCSMDTSD 120 (SEQ ID NO: 38)

>patp:R15106 hCG/bLH chimera, D10 - *Homo sapiens*, 145 aa.
Plus Strand HSPs:

Score = 188 (66.2 bits), Expect = 5.0e-14, P = 5.0e-14
Identities = 40/101 (39%), Positives = 58/101 (57%), Frame = +1
Query: 76 SSGNLRTFVGCAVREFTFLAKKPGCRG-LRITTDACWGRCETWEK--PILEPPYIEAHR 246
S G LR C T A+K C + TT C G C + ++ P++ PP + R
Sbjct: 1 SRGPLRPL--CQPINATLAAEKEACPVCITFTTICAGYCPMSMKRVLVPILPPMPQ---R 55

Query: 247 VCTYNETKQVTVKLPNCAPGVDPFYTYTPVAIRCDCGACSTATTE 378 (SEQ ID NO: 39)
VCTY+E + +V+LP C PGVDP ++PVA+ C CG C ++T+ (SEQ ID NO: 40)
Sbjct: 56 VCTYHELRFASVRLPGCPPGVDPVMSFPVALSCHCGPCRLSSTD 99 (SEQ ID NO: 41)

>patp:W65110 Equine chorionic gonadotropin beta-chain protein - *Equus caballus*, 169 aa.

Plus Strand HSPs:
Score = 175 (61.6 bits), Expect = 1.2e-12, P = 1.2e-12
Identities = 43/116 (37%), Positives = 60/116 (51%), Frame = +1
Query: 31 MALLLLAGYGCVLGASSGNLRTFVGCAVREFTFLAKKPGCR-GLRITTDACWGRCETWEK 207
+ L +L G V AS G LR C T A+K C + TT C G C + +
Sbjct: 7 LLLWMLLSVGGVW-ASRGPLRPL--CRPINATLAAEKEACPICITFTTICAGYCPMSMR 63

Query: 208 PILEPPYIEAHR-VCTYNETKQVTVKLPNCAPGVDPFYTYTPVAIRCDCGACSTATTE 378 (SEQ ID NO: 42)
+ P + A + VCTY E + +++LP C PGVDP ++PVA+ C CG C TT+ (SEQ ID NO: 43)
Sbjct: 64 VM--PAALPAIPQPVCTYRELRFASIRLPGCPPGVDPVMSFPVALSCHCGPCQIKTTD 119 (SEQ ID NO: 44)

Fig. 7B

ClustalW alignment for NOVGN:

Based on this alignment, black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties); greyed amino acid residues can be mutated to a residue with comparable steric and/or chemical properties without altering protein structure or function (e.g. L to V, I, or M); non-highlighted amino acid residues can potentially be mutated to a much broader extent without altering structure or function.

GTHB_CYPCA	MGTPVKLWVRNHILFSVVLLHVAQSS---YLPPCEPVNETVAVEKEGCPKCLVLQHTI
Q98849_OTHB2_GOLDFISH	MGTPVKLWV---LFSVIVLHVAQSS---YLPPCEPVNETVAVEKEGCPKCLVLQHTI
LSHB_BOVIN	MEMFOGLW---LLLGVAQVWASRGV---LRPLCOPINATLAEEKACPVCTTFTTSI
LSHB_SHEEP	MEMFOGLW---LLLGVAQVWASRGV---LRPLCOPINATLAEEKACPVCTTFTTSI
novel_gonadotropin	MKLAFLLGPMALLLACVGCVLGASSGNLRTFVGCVAVREFIFLAKKPGGCG---IRITIDA

GTHB_CYPCA	CSGHCLT-KEPVYKSPSTMYOHVCTYRDVRYETVRLDCPPGVDPHITYPVALSCDCSL
Q98849_GTHB2_GOLDFISH	CSGHCLT-KEPVYKSPSTMYOHVCTYRDVRYETVRLDCPPGVDPHITYPVALSCDCSL
LSHB_BOVIN	CACYCPS-MKRVLPVILPPMPORVCTYHELRFASVRLEGCPPGVDEPMVSEPVVALSCHCGP
LSHB_SHEEP	CACYCLS-MKRVLPVILPPMPORVCTYHELRFASVRLEGCPPGVDEPMVSEPVVALSCHCGP
novel_gonadotropin	CWGRCTWEKPILEPPHTEAHRVCTYNETKQVTVKLPNCAFGVDPFYTYPVAIRCDCGA

GTHB_CYPCA	CFMDTSD-----CT---IESLOPDFQMSQ-REDFIVY-----
Q98849_GTHB2_GOLDFISH	CFMDTSD-----CT---IESLOPDFQMSQ-REDFIVY-----
LSHB_BOVIN	CRSSSTD-----CG---GPRTQPLACDHPPLDILFL-----
LSHB_SHEEP	CRSSSTD-----CG---GPRTQPLACDHPPLDILFL-----
novel_gonadotropin	CSTATTELRLMPGEAAVALGFWCQRRRCQSRTTGTRWRHAAVRDKVSLLKAVDGNWNGLLG

GTHB_CYPCA	-----	(SEQ ID NO: 45)
Q98849_GTHB2_GOLDFISH	-----	(SEQ ID NO: 46)
LSHB_BOVIN	-----	(SEQ ID NO: 47)
LSHB_SHEEP	-----	(SEQ ID NO: 48)
novel_gonadotropin	DPASSQGLSASSCTPVFPLAFQIDSASGKVGNFSSKQTFIFSSAEITLGGT	(SEQ ID NO: 49)

Fig. 8

NOVINTRA A cDNA sequence:

Regions 116708 to 116812(1-105bp),117121 to 117248(106-233p),and 117529 to 117778 (234-483bp).

CACTGTCACTGTTTCAGAATTAAATATGCAGACCAGAAGGCTCTATACACAAGAG
 ATGGCCAGCTGCTGGTGGGAGATCCTGTTGCAGACAAGCTGTGCAGAGAAGATC
 TGCATACTTCTTAACAGAGGCTTGGCCCGACCAAGGTCCCATTTTCTGGGGATC
 CAGGGAGGGAGCCGCTGCCTGGCATGTGTGGAGACAGAAGAGGGCCCTTCCCTACA
 GCTGGAGCCATCCACCTTCCCCCACAGGATGTGAACATTGAGGAAGTGTACAAAG
 GTGGTGAAGAGGCCACACGCTTACCTTCTCCAGAGCAGCTCAGGCTCCGCCTTCA
 GGCTTGAGGCTGCTGCCTGGCCTGGCTGGTTCTGTGTGGCCCGGCAGAGCCCCAGC
 AGCCAGTACAGCTCACCAAGGAGAGTGAGCCCTCAGCCCGTACCAAGTTTACTTTG
 AACAGAGCTGGTAGGGAGACAGGAACTGC (SEQ ID NO: 7)

Fig. 9A

NOVINTRA A Protein sequence:

LSYCFRIKYADOKALYTRDGOLLVGDVPVADNCCAEEKICILPNRGLARTKVPIFLGIQGGG
 RCLACVETEEGPSLQLEPSTLPPQDVNIEELYKGGEATRFTFFQSSSGSAFRLEAAAWP
 GWFLCGPAEPQQPVLTKSEPSARTKFYFEQSW (SEQ ID NO: 8)

Fig. 9B

BlastN for NOVINTRA A:

gb:GENBANK-ID:AF072476|acc:AF072476 Equus caballus interleukin-1 receptor
antagonist secretory form (IL-lra) gene, partial cds - Equus caballus,
221
bp.

Top Previous Match Next Match

Length = 221

Plus Strand HSPs:

Score = 321 (48.2 bits), Expect = 8.1e-08, P = 8.1e-08

Identities = 147/218 (67%), Positives = 147/218 (67%), Strand = Plus / Plus

Query: 253 AGGATGTGAACATTGAGGAAGTGTACAA-AGGTGGTGAAGAGCCACAGCCTTCACCTTC 311
AGG GT AACAT GA CTG CAA A G GA GAG CA CGCTTCACCTTC
Sbjct: 4 AGGCAGTTAACATCACTGACCTGAGCAAGAACAAG-GAGGAGAACAAGCGCTTCACCTTC 62

Query: 312 TTCCAGAGCAG-CTCAGGCTCCGCCTTCAGGCTT-GAGGCTGCTGCCTGGCCTGGCTGGT 369
TCC G CA C GGC CC CC CAG CTT GAG CTGC GCCTG CCTGGCTGGT
Sbjct: 63 ATCC-GCTCAAACAGTGGCCCCACCACCAG-CTTCGAGTCTGCCGCTGCCCTGGCTGGT 120

Query: 370 TCCTGTGTGGCCCGGCAG-AGCCCCAGCAGCCAGTACAGC-TCACCAAGGAG---AGTGA 424
TCCT TG CG CAG AG C A C GCC GT CAGC TCACCA AG A GA
Sbjct: 121 TCCTCTGCACGGCG-CAGGAGGCAGACCGGCCCGT-CAGCCTCACCAACAAGCCCAAAGA 178

Query: 425 GCCCT-CAGCCCGT-ACCAAGTTTACTTTGAACAGAGCTGGTAG 467 (SEQ ID NO: 50)
G CCT CA GT ACCAAGTT TACTT A AG C GTAG (SEQ ID NO: 51)
Sbjct: 179 GTCCTTCATG--GTCACCAAGTTCTACTTCCAGGAGGACCAGTAG 221 (SEQ ID NO: 52)

Fig. 10A

BlastX for NOVINTRA A:

ptnr:TREMBLNEW-ACC:CAB59831 IL-1L1 PROTEIN - Mus musculus (Mouse), 155 aa.

Top Previous Match Next Match

Length = 155

Plus Strand HSPs:

Score = 309 (108.8 bits), Expect = 8.0e-27, P = 8.0e-27
Identities = 70/149 (46%), Positives = 93/149 (62%), Frame = +3

Query: 12 CFRIKYADQKALYTRDGQLLVGDPVADNCC-AEKICILPNRGLARTKVPIFLGIQGGSRC 188
CFR+K + K LY + QLL G A+ E+I ++PNR L + P+ LG+QGG+C
Sbjct: 8 CFRMKDSALKVLYLHNNQLLAGLHAEKVIKGEETISVVPNRALDASLSPVILGVQGGQC 67

Query: 189 LACVETEEGPSLQLEPSTLPPQDVNIEELYKGGEATRTFFQSSSGSAFRLEAAAWPGW 368
L+C TE+GP L+LEP VNI ELY G +E+ FTF++ G E+AA+PGW
Sbjct: 68 LSC-GTEKGPILKLEP-----VNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGW 119

Query: 369 FLCGPAEPQQPVLTKSEPSAR----TKFYFEQ 458 (SEQ ID NO: 53)
FLC E QPV+LT+ E A T FYF+Q (SEQ ID NO: 54)
Sbjct: 120 FLCTSPEADQPVRILTQIPEDPAWDAPITDFYFQQ 153 (SEQ ID NO: 55)

>ptnr:SPTREMBL-ACC:Q9UBH0 FIL1 DELTA (INTERLEUKIN-1 LIKE PROTEIN 1)
(INTERLEUKIN-1 RECEPTOR ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA) - Homo
sapiens (Human), 155 aa.

Plus Strand HSPs:

Score = 285 (100.3 bits), Expect = 4.3e-24, P = 4.3e-24
Identities = 67/149 (44%), Positives = 89/149 (59%), Frame = +3

Query: 12 CFRIKYADQKALYTRDGQLLVGDPVADNCC-AEKICILPNRGLARTKVPIFLGIQGGSRC 188
CFR+K + K LY + QLL G A E+I ++PNR L + P+ LG+QGG+C
Sbjct: 8 CFRMKDSALKVLYLHNNQLLAGLHAGKVIKGEETISVVPNRWLDASLSPVILGVQGGQC 67

Query: 189 LACVETEEGPSLQLEPSTLPPQDVNIEELYKGGEATRTFFQSSSGSAFRLEAAAWPGW 368
L+C +E P+L LEP VNI ELY G +E+ FTF++ G E+AA+PGW
Sbjct: 68 LSCGVGQE-PTLTLEP-----VNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGW 119

Query: 369 FLCGPAEPQQPVLTKSEPSAR----TKFYFEQ 458 (SEQ ID NO: 56)
FLC E QPV+LT+ E T FYF+Q (SEQ ID NO: 57)
Sbjct: 120 FLCTVPEADQPVRILTQLPENGGWNPITDFYFQQ 153 (SEQ ID NO: 58)

Fig. 10B

ClustalW for NOVINTRA A:

Based on this alignment, black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties); greyed amino acid residues can be mutated to a residue with comparable steric and/or chemical properties without altering protein structure or function (e.g. L to V, I, or M); non-highlighted amino acid residues can potentially be mutated to a much broader extent without altering structure or function.

Sequences used:

- 1) X86458spoil1 (cDNA encoding a human spoil-I protein); X86459spoil2 (cDNA encoding a human spoil-II protein); X89432-illdelta (human IL-1 delta encoding cDNA); Q14628 (intracellular IL-I receptor antagonist type II-human); G512010illbeta (ovine IL-1 beta - pig)

```

X86458spoil1      -----DNHTMRGTPGDA-----DGG--GRAVYQS-----
X86459spoil2      -----DNHTMRGTPGDA-----DGG--GRAVYQSSESNAVGMGLWRLRPSALTLSPV
X89432-illdelta   -----MALADLYEEG-----GGG--CGEGEDNADSK-----E-----
Q14628
illbeta-1DNA
G512010illbeta    MATVPEPINEVMAYYSDENELLFEVDGPKQMKSCQHLDLGSMGDGNIQLQISHQLYNKS

X86458spoil1      -----MCKPITGTLNDLNCQVWILLOGNLVAVPRSDS--VTPVIVAVIT
X86459spoil2      EAPAFSAPLCTLPFPVCKPITGTLNDLNCQVWILLOGNLVAVPRSDS--VTPVIVAVIT
X89432-illdelta   -----MVLSCALCFMKDSALKVLYTHNNQLACGLHA-----GRVILKGEET
Q14628            -----TICRPSGRKSSKMOAFRIWDNOKTFYLRNNOLVAGYLOG--PNVNLKEKI
illbeta-1DNA      -----GPSALSYCFRIKYADOKALYTRDQQLLVGDPVA-----DNCCAEKI
G512010illbeta    FRQVSVIVAMEKLRSRAYEHVFRDDILRSILSFI FEEEPVIFETSSDELLCDAAVQSVK

X86458spoil1      CKYPEAL-----EQGRGDPYILGIONPEM
X86459spoil2      CKYPEAL-----EQGRGDPYILGIONPEM
X89432-illdelta   SVWPNRW-----LDASLSPVILGVCGGCSQ
Q14628            DVWPP-----IEPHALFLGIHGGRM
illbeta-1DNA      CIEPNRG-----LARTKVPIFLGICGCSR
G512010illbeta    CKIQREQKSLVLDSPCVLKALHLLSQEMSREVVFCMSFVQGBERDNKIPVALGIRDKNL

X86458spoil1      CLYCEKVGEPTLOLKE-----QKIMDLYGQPEPVKPELFYRAKTCRTSILESVAEPD
X86459spoil2      CLYCEKVGEPTLOLKE-----QKIMDLYGQPEPVKPELFYRAKTCRTSILESVAEPD
X89432-illdelta   CLSCG-VCQEPITILEP-----VNIMELYLGAKESKSETFYRRDMCLTSSESAAAPG
Q14628            CLSCVKSCQETRLQLEA-----VNITDLSENKQDKREAFIRSDSGPITSFESAACPG
illbeta-1DNA      CLACVETEEGSLQLEPSTLPPQDVNIEELYKGGFEATRETFQSSSCSAFRLEAAAPG
G512010illbeta    YLSCVKKGEPTLOLEE-----VDPKVYPKRNMEKRFVFYKTEIKNIVEFESVLYEN

X86458spoil1      WFLASS-KRDOPHITSELCKS-----YNTAFELNIND- (SEQ ID NO: 59)
X86459spoil2      WFLASS-KRDOPHITSELCKS-----YNTAFELNIND- (SEQ ID NO: 60)
X89432-illdelta   WFLCTVPEADOPVRLTQLPENGOWNAPIIDEIFQCC- (SEQ ID NO: 61)
Q14628            WFLCTAMEADOPVSLINMPDEG---VMVIKFFYQSEDE- (SEQ ID NO: 62)
illbeta-1DNA      WFLCGPAEPQOPVOLTKESEPS-----ARTIKFFYEQSW- (SEQ ID NO: 63)
G512010illbeta    WFLSTQTEKPVFLGRFRGQ---DIIDERMETLSP (SEQ ID NO: 64)

```

Fig. 11

NOVINTRA B cDNA sequence:

Regions 116968 to 117028 (1-61bp), 104067 to 104164 (62-159bp), 101958 to 102098 (160-300bp), and 100915 to 101134 (301-520bp) of genomic clone (-frame).

ATGGGCACACCTGGCCTGGCCCTGCATGCAGACTGGACGGTGAGCCAGGACTTCTG
CAGGACACCCAAATCCTATGCTATTCGTGATTCTCGACAGATGGTGTGGGTCCTGAG
TGGAAATTCTTTAATAGCAGCTCCTCTTAGCCGCAGCATTAAAGCCTGTCACTCTTCAT
TTAATAGCCTGTAGAGACACAGAATTCAGTGACAAGGAAAAGGGTAATATGGTTTA
CCTGGGAATCAAGGGAAAAGATCTCTGTCTCTTCTGTGCAGAAATTCAGGGCAAGCC
TACTTTGCAGCTTAAGGAAAAAATATCATGGACCTGTATGTGGAGAAGAAAGCAC
AGAAGCCCTTTCTCTTTTCCACAATAAAGAAGGCTCCACTTCTGTCTTTCAGTCAGT
CTCTTACCCTGGCTGGTTCATAGCCACCTCCACCACATCAGGACAGCCCATCTTTCTC
ACCAAGGAGAGAGGCATAACTAATAACACTAACTTCTACTTAGATTCTGTGGAATA
AATCCAGC (SEQ ID NO: 9)

Fig. 12A

NOVINTRA B Protein sequence:

MGTPGLALHADWTVSQDFCRTPKSYAIRDSRQMWWVLSGNSLIAAPLSRSIKPVTLHLI
ACRDTEFSDKEKGNMVLGIKGDLCFCAEIQ GKPTLQLKEKNIMDL YVEKKAQKPFL
FFHNKEGSTSVFQSVSPGWFIATSTTSGQPIFLTKERGITNNTNFYLD SVE (SEQ ID NO: 10)

Fig. 12B

BlastN for NOVINTRA B:

gb:GENBANK-ID:PIGIRAP|acc:L38849 Sus scrofa (clone p0328w) IRAP1 mRNA,
complete cds - Sus scrofa, 563 bp (RNA).

Top Previous Match Next Match

Length = 563

Plus Strand_HSPs:

Score = 309 (46.4 bits), Expect = 1.1e-07, P = 1.1e-07

Identities = 197/331 (59%), Positives = 197/331 (59%), Strand = Plus / Plus

Query: 169 CATTTAATAGCCTGTA-GAGAC-ACAGAATTCAGTGACAAGGAAAAGGGTAATATGGTTT 226
CA TA TA CTG A GAGA A AGA T GTG C G AG T AT T GT T

Sbjct: 217 CAAATACTAAACTGGAAGAGAAGATAGATGTG-GTGCCT--GTTGAGCCTCATTTCGTGT 273

Query: 227 ACCTGGGAATCAAGGGAAAAGATCTCTGTCTCTTCTGTGCAGAAATTCAGGGCAAGCC-T 285
CCTGGG ATC A GGA A CT TG CT T CTGTG AA T C GG A G T

Sbjct: 274 TCCTGGGGATCCATGGAGGGAAGCTGTGCCTGTCTGTGTC-AAGT-CTGGTGATGAGAT 331

Query: 286 -ACTTTGCAGCTTAAGGAAAAAATATCATGGACCTGTATGTGGAGAAGAAAGCAC-AGA 343
A T CAG T A G A AA ATCA GACCTG A GA AG AGCA A A

Sbjct: 332 GAAGCTCCAGTTGGACGCAGTTAACATCACAGACCTG-AGAAAGAACAGCGAGCAGGACA 390

Query: 344 AGCCCTTTCTCTTTTCCACAATAA-AGAAGGCTCCACTTCTGTCTTTTCAGTCAGTCTCT 402
AGC CTT CTT TCC C A AG GGC CCAC C CTTT AGTCAG C C

Sbjct: 391 AGCGCTTCACCTTCATCCGCTCCGACAGT-GGCCCCACCACCAGCTTTGAGTCAGCCGCC 449

Query: 403 TACCCTGGCTGGTTTCATAGCCACCTCCACCACAT-CAGGACAGCCCATCTTTCTCACCAA 461
T CCTGGCTGGTTC T CAC T CAC A A CAG CAGCC T CTCACCAA

Sbjct: 450 TGTCTGGCTGGTTCTCTGCAC-TGCACTAGAGGCAGACCAGCCTGTTGGCCTCACCAA 508

Query: 462 GGAGAG-AG-GCATAACT-AATAACACTAACTTCTACTT 497 (SEQ ID NO: 65)

G A GCA T AA CAC AA TTCTACTT (SEQ ID NO: 66)

Sbjct: 509 CACGCCCAAAGCAGCCGTCAAGGTCACCAAGTTCTACTT 547 (SEQ ID NO: 67)

Fig. 13A

BlastX for NOVINTRA B:

>ptnr:SPTREMBL-ACC:Q9UHA5 FIL1 ETA - Homo sapiens (Human), 157 aa.
Plus Strand HSPs:

Score = 777 (273.5 bits), Expect = 3.2e-76, P = 3.2e-76
Identities = 149/149 (100%), Positives = 149/149 (100%), Frame = +1

Query: 64 PKSYAIRDSRQMVVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIGK 243
PKSYAIRDSRQMVVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIGK
Sbjct: 9 PKSYAIRDSRQMVVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIGK 68

Query: 244 KDLCLFCAEIQ GKPTLQLKEKNIMDLYVEKKAQKPFLFFHNKEGSTSVFQSVSYPGWFIA 423
KDLCLFCAEIQ GKPTLQLKEKNIMDLYVEKKAQKPFLFFHNKEGSTSVFQSVSYPGWFIA
Sbjct: 69 KDLCLFCAEIQ GKPTLQLKEKNIMDLYVEKKAQKPFLFFHNKEGSTSVFQSVSYPGWFIA 128

Query: 424 TSTTSQGPIFLTKEGKITNNTNFYLDSE 510 (SEQ ID NO: 68)
TSTTSQGPIFLTKEGKITNNTNFYLDSE (SEQ ID NO: 69)
Sbjct: 129 TSTTSQGPIFLTKEGKITNNTNFYLDSE 157 (SEQ ID NO: 70)

>ptnr:SPTREMBL-ACC:Q9NZH7 INTERLEUKIN-1 HOMOLOG 2 - Homo sapiens (Human), 164 aa.
Plus Strand HSPs:

Score = 411 (144.7 bits), Expect = 1.9e-37, P = 1.9e-37
Identities = 80/85 (94%), Positives = 81/85 (95%), Frame = +1

Query: 64 PKSYAIRDSRQMVVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIGK 243
PKSYAIRDSRQMVVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIGK
Sbjct: 9 PKSYAIRDSRQMVVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIGK 68

Query: 244 KDLCLFCAEIQ GKPTLQLKEKNIMD 318 (SEQ ID NO: 71)
KDLCLFCAEIQ GKPTLQLK + D (SEQ ID NO: 72)
Sbjct: 69 KDLCLFCAEIQ GKPTLQLKLQGSQD 93 (SEQ ID NO: 73)

>ptnr:TREMBLNEW-ACC:AAF02757 INTERLEUKIN-1 RECEPTOR ANTAGONIST HOMOLOG
- Homo sapiens (Human), 155 aa.

Top Previous Match Next Match
Plus Strand HSPs:

Score = 197 (69.3 bits), Expect = 5.9e-15, P = 5.9e-15
Identities = 52/147 (35%), Positives = 76/147 (51%), Frame = +1

Query: 73 YAIRDSRQMVVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIGKDL 252
+ ++DS V L N L+A L K + I+ + D ++ LG++G
Sbjct: 9 FRMKDSALKVLYLHNNQLLAGGLHAG-KVIKGEIISVVPNRWLDASLSPVI-LGVQGSQ 66

Query: 253 CLFCAEIQ GKPTLQLKEKNIMDLYVEKKAQKPFLFFHNKEGSTSVFQSVSYPGWFIAATST 432
CL C Q +PTL L+ NIM+LY+ K K F F+ G TS F+S +YPGWF+ T
Sbjct: 67 CLSCGVGQ-EPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVP 125

Query: 433 TSGQPIFLT--ERGITNN--TNFYLDSE 510 (SEQ ID NO: 74)
+ QP+ LT+ E G N T+FY + (SEQ ID NO: 75)
Sbjct: 126 EADQPVRLTQLPENGGWNAPITDFYFQQCD 155 (SEQ ID NO: 76)

Fig. 13B

ClustalW for NOVINTRA B:

Based on this alignment, black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties); greyed amino acid residues can be mutated to a residue with comparable steric and/or chemical properties without altering protein structure or function (e.g. L to V, I, or M); non-highlighted amino acid residues can potentially be mutated to a much broader extent without altering structure or function.

Sequences used:

2) X86459spoil2 (cDNA encoding a human spoil-II protein; Q14628 (intracellular IL-1 receptor antagonist type II-human); AAF02757 (intracellular IL-1 receptor antagonist type II-human); G512010; (OVINE IL-1 BETA - Pig)

Multiple Alignment:

```

illbeta2DNA      -----MC1EPCLALHADWTVS2CD-----
X86459spoil2     -----DNHTMR3EP4CDADGGGRAVY5QSSSEN
Q14628           -----MALADLYEE6GGGGGEGEDNADSK7E-
AAF02757         -----
G512010illbeta   MATVPEPINEVMAYYSDENELLFEVDGPKQMKSC8TQHLDL9CS10MDGNIQLQISH11QLYNKS

illbeta2DNA      -----F12ORT-----PKSYAIR-----
X86459spoil2     AVGMGLWRLRPSALTLSPEAPAFSAPLC13TLFPFPVCK14-PITGTIN-----
Q14628           -----TI15CRPSGRKSSK16-MQAFRIW-----
AAF02757         -----MVL17SG-ALCFRMK-----
G512010illbeta   FRQVVSIVIVAMEKLRSRAYEHVFRDDDLRSILSFIFE18EE19VI20ETSSDELLCDAAVQSVK

illbeta2DNA      ----DSROM21VVLSGN22SLIA23APT24SRSIKP25V26LHI27ACRDTEFS28DK-EKGNM29V30LG31IK32GD
X86459spoil2     ----DLNQ33QV34WT35LQ36QNL37VAV38PRSDSV39TP40VAV41NTCKY42PEALEQ-GRGDE43PL44GI45ONPE
Q14628           ----DVN46Q47TEY48LRN49N50LVAG51YLQ--GPN52VN53LEEKIDV54VP-----IEPHAL55LG56IH57CGK
AAF02757         ----DSALK58V59LYL60HN61QL62LA63GLH--AGK64VI65KGE66EISV67ENR68WLD-ASLSE69VIL70GV71Q72GS
G512010illbeta   CKLQ73DRE74Q75SLV76LD77S-PCVL78KAL79HLL80SQEMS81RE82V83FC84MS85FV86Q87GER88DN89KI90PVAL91GI92RDKN

illbeta2DNA      ECL93FC94AEIO95CK96PT97LQ98LKE99KNIM100DLY101VEK102KAQ103KP104EF105HN106KEG107ST108SV109EQ110SV111PG112WF113IA114TS
X86459spoil2     MCLY115CEK116VGE117QPT118LQ119LKE120QIM121DLY122GQ123PE124VP125KP126EF127YRA128KT129GR130TS131LES132VAF133PD134WF135IA136SS
Q14628           MCL137SC138VK139SG140DET141RLQ142LEAV143NIT144DLSEN145RK146QDK147RA148FT149RS150DS151GP152TI153EF154SA155AC156PG157WF158ET159CTA
AAF02757         QCL160SCG161-VG162QEP163TL164ILE165PVNIM166ELY167LGAK168ESK169SFT170YRR171DM172GL173TS174EF175SA176AY177PG178WF179ET180CTV
G512010illbeta   EYL181SCV182KK183GD184PT185LQ186LEEV187DPK188VYP-KRN189ME190KRF191VYK192TEI193KN194VE195FES196VLY197PN198WY199IST200S

illbeta2DNA      TTSC201Q202PI203FLIK204ER--G--IT205NN206IN207FY208LD209SVE- (SEQ ID NO: 77)
X86459spoil2     KRD210-Q211PI212IL213SEL--G--K214SYNT215AF216EL217NIND- (SEQ ID NO: 78)
Q14628           MEAD218Q219PV220SL221IN222MP223DEG---VM224V225KE226Y227FQ228EDE- (SEQ ID NO: 79)
AAF02757         PEAD229Q230PV231RL232TQ233LPEN234CG235WN236AP237IT238DF239YF240QQ241CD- (SEQ ID NO: 80)
G512010illbeta   QIEEK242PV243FL244GR245FR--G--Q246DI247TD248ERM249ET250LSP (SEQ ID NO: 81)

```

Fig. 14

NOVINTRA C cDNA sequence:

Region 168700 to 168880 (1-181bp), 169967 to 170118 (182-331bp) and 170635 to 170694 (332-391bp) of the genomic clone (- frame).

GATATCAATCATCGGGTGTGGGTCTTTCAGGACCAGACGCTCATAGCAGTCCCGAGG
AAGGTGTTCCCAGTCACTATTGCCTTAATCTCATGCGACATGTGGAGACCCTTGAG
AAAGACAGAGGGAACCCCATCTACCTGGGCCTGAATGGACTCAATCTCTGCCTGAT
GTGTGCTAAAGTCGGGGACCAGCCACACTGCAGCTGAAGCTTCAGGAAAAGGATA
TAATGGATTTGTACAACCAACCCGAGCCTGTGAAGTCCTTTCTCTTCTACCACAGCC
AGAGTGGCAGGAACCTCCACCTTCGAGTCTGTGGCTTTCCTGGCTGGTTCATCGCTG
TCAGCTCTGAAGGAGGCTGTCTCTCATCCTTACCCAAGAACTGGGGAAAG (SEQ ID NO: 11)

Fig. 15A

NOVINTRA C Protein sequence:

DINHRVWVLQDQTLIAVPRKVFVPTIALISCRHVETLEKDRGNPIYLGLNGLNLCLMCAK
VGDQPTLQLKLQEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGC
PLILTQELGK (SEQ ID NO: 12)

Fig. 15B

BlastN for NOVINTRA C:

gb:GENBANK-ID:PIGIRAP|acc:L38849 Sus scrofa (clone pO328w) IRAP1 mRNA,
complete cds - Sus scrofa, 563 bp (RNA).

Top Previous Match Next Match

Length = 563

Minus Strand-HSPs:

Score = 274 (41.1 bits), Expect = 5.6e-06, P = 5.6e-06

Identities = 150/244 (61%), Positives = 150/244 (61%), Strand = Minus / Plus

Query: 258 TCTACCTGGGCTGAATGGACTCAATCTCTGCCTGATGTGTGCTAAAGTCGGG-GACCAG 200
T T CCTGGG T ATGGA AA CT TGCCTG TGTG T AAGTC GG GA AG
Sbjct: 271 TGTTCCTGGGATCCATGGAGGGAAGCTGTGCCTGTCTGTG-TCAAGTCTGGTGATGAG 329

Query: 199 CCCACACTGCAGCTGAAGCTTCAGGAAAAGGATATAATGGATTTGTACAACCAACC-CGA 141
A CT CAG TG A C CAG AA AT A GA TG A AA AAC CGA
Sbjct: 330 ATGAAGCTCCAGTTGGA-CG-CAGTTAAC----ATCACAGACCTG-AGAAAGAACAGCGA 382

Query: 140 GCCTGTGAAGTCCTTTCTCTTCTACCACAGCCAGAGTGGCAGGAACCTCCACCTTCGAGTC 81
GC G AAG CTT CTTC CC C C A AGTGGC A C CCA CTT GAGTC
Sbjct: 383 GCAGGACAAGCGCTTCACCTTCATCCGCTCCGACAGTGGCCCCACCACCAGCTTTGAGTC 442

Query: 80 TGTGGCTTTCCCTGGCTGGTTCATCGCTGT-CAGCTCTGAAGG-AGGCTGTCTCTCATC 23
G GC T CCTGGCTGGTTC TC TG C GC CT AGG AG C CCT T C
Sbjct: 443 AGCCGCCTGTCTGGCTGGTTCCTC--TGCACTGCACTAGAGGCAGACCAGCCTGTTGGC 500

Query: 22 CTTACCCA 15 (SEQ ID NO: 82)
CT ACC A (SEQ ID NO: 83)
Sbjct: 501 CTCACCAA 508 (SEQ ID NO: 84)

Fig. 16A

BlastX for NOVINTRA C:

>ptnr:SPTREMBL-ACC:Q9UHA7 FIL1 EPSILON - Homo sapiens (Human), 158 aa.
Plus Strand HSPs:

Score = 646 (227.4 bits), Expect = 2.4e-62, P = 2.4e-62
Identities = 126/130 (96%), Positives = 127/130 (97%), Frame = +1

Query: 1 DINHRVWVLQDQTLIAVPRK--VFPVTIALISCRHVETLEKDRGNPIYLGNGNLNCLMC 174
DINHRVWVLQDQTLIAVPRK + PVTIALISCRHVETLEKDRGNPIYLGNGNLNCLMC
Sbjct: 17 DINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGNGNLNCLMC 76

Query: 175 AKVGDQPTLQLKLQEKDMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIASSEG 354
AKVGDQPTLQLK EKDMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIASSEG
Sbjct: 77 AKVGDQPTLQLK--EKDMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIASSEG 134

Query: 355 GCPLILTQELGK 390 (SEQ ID NO: 85)
GCPLILTQELGK (SEQ ID NO: 86)
Sbjct: 135 GCPLILTQELGK 146 (SEQ ID NO: 87)

>ptnr:SPTREMBL-ACC:Q9NZH8 INTERLEUKIN-1 HOMOLOG 1 - Homo sapiens, 169 aa.

Plus Strand HSPs:

Score = 416 (146.4 bits), Expect = 5.7e-38, P = 5.7e-38
Identities = 82/130 (63%), Positives = 101/130 (77%), Frame = +1

Query: 1 DINHRVWVLQDQTLIAVPRK--VFPVTIALISCRHVETLEKDRGNPIYLGNGNLNCLMC 174
D+N +VW LQ Q L+AVPR V PVT+A+I+C++ E LE+ RG+PIYLG+ +CL C
Sbjct: 29 DLNQVWTLQGQNLVAVPRSDSVTPVTAVITCKYPEALEQGRGDIYLGQNPCLYC 88

Query: 175 AKVGDQPTLQLKLQEKDMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIASSEG 354
KVG+QPTLQLK E+ IMDLY QPEPVK FLFY +++GR ST ESVAFP WFIA SS+
Sbjct: 89 EKVGQPTLQLK--EQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIA-SSKR 145

Query: 355 GCPLILTQELGK 390 (SEQ ID NO: 88)
P+ILT ELGK (SEQ ID NO: 89)
Sbjct: 146 DQPIILTSELGK 157 (SEQ ID NO: 90)

>ptnr:SWISSPROT-ACC:P25085 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN
PRECURSOR (IL-1RA) (IL-1RN) (IRAP) - Mus musculus (Mouse), 178 aa.

Top Previous Match Next Match

Minus Strand HSPs:

Score = 173 (60.9 bits), Expect = 2.1e-12, P = 2.1e-12
Identities = 35/81 (43%), Positives = 50/81 (61%), Frame = -1

Query: 259 IYLGNGNLNCLMCAKVGDPPTLQLKLQEKDMDLYNQPEPVKSFLFYHSQSGRNSTFES 80
++LG++G LCL CAK GD ++L+L+E +I DL E K F F S+ G ++FES
Sbjct: 82 VFLGIHGGKLCSCAKSGDD--IKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPPTS FES 139

Query: 79 VAFPGWFIASSEGCGPLILT 17 (SEQ ID NO: 91)
A PGWF+ + E P+ LT (SEQ ID NO: 92)
Sbjct: 140 AACPGWFLCTTLEADRPVSLT 160 (SEQ ID NO: 93)

Fig. 16B

ClustalW for NOVINTRA C:

Based on this alignment, black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties); greyed amino acid residues can be mutated to a residue with comparable steric and/or chemical properties without altering protein structure or function (e.g. L to V, I, or M); non-highlighted amino acid residues can potentially be mutated to a much broader extent without altering structure or function.

Sequences used:

- 1) IL1X_MOUSE: Locus - IL1X_MOUSE; Accession - P25085; PID - g124313
- 2) IL1X_HORSE: Locus - IL1X_HORSE; Accession - 018999; PID - g6166230
- 3) AAF02757_HUMAN: Locus - AF186094_1; Accession - AAF02757; PID - g6049805

IL1X_MOUSE	MEICWGPYSHLISLLILLFHSEAACRPSGKRPCKMQAFRIWDITNOKTFYLRNNQLIAGY
IL1X_HORSE	MEIRRRSVRHLIS-LLLFLEYSETACHPLGKRPCKMQAFRIWDVNOKTFYMRNNQLVAGY
AAF02757_Human	-----MVLSCAIC-----FRMKDSALKVLYLHNNQLLAGG
Novel_IL1	-----DINHRVWVLDQDTLIAVP
IL1X_MOUSE	LCGPNIKLE---EKIDMVP-----IDLSVFLGIHGGKLCCLCAKSCDEIKLOLEEVN-
IL1X_HORSE	LQESNTKIQ---EKIDVVP-----IDPDALFLGLHCRKLCIACVKSCDEIRFQLEAVN-
AAF02757_Human	LHAGKVIKG---EELSVVENRWLDASLSPVILGVCGGSQCLSCG-VGQEPITLTLEPVN-
Novel_IL1	RKVFPVTEALISCRHVETLEK---DRGNPIYLGILNGLNLCIMCAKVGDDPTLOLKLQEK
IL1X_MOUSE	-ITDLSKNKEEDKRFTEIRSEKCPTESFESAACPGWFLCTQLLEADRPVSLNTIPPE---P
IL1X_HORSE	-ITDLSKNKEENKRFTEIRNSGPTESFESAACPGWFLCTAQEADRPVSLTNKPKKE---S
AAF02757_Human	-IMELYLGAKESKSEFYRRDMGLTSFESAAYPGWFLCTVPEADQPVRLTQLPENGAWN
Novel_IL1	DIMDIYNQPEPVKSELYHSQSGRNSIFESVAFPGWEIAVSSEEGCPILITQELGK----
IL1X_MOUSE	LEVTKFYFOEDQ (SEQ ID NO: 94)
IL1X_HORSE	FMVTKFYLOEDQ (SEQ ID NO: 95)
AAF02757_Human	APETDFYFQQCD (SEQ ID NO: 96)
Novel_IL1	----- (SEQ ID NO: 97)

Fig. 17

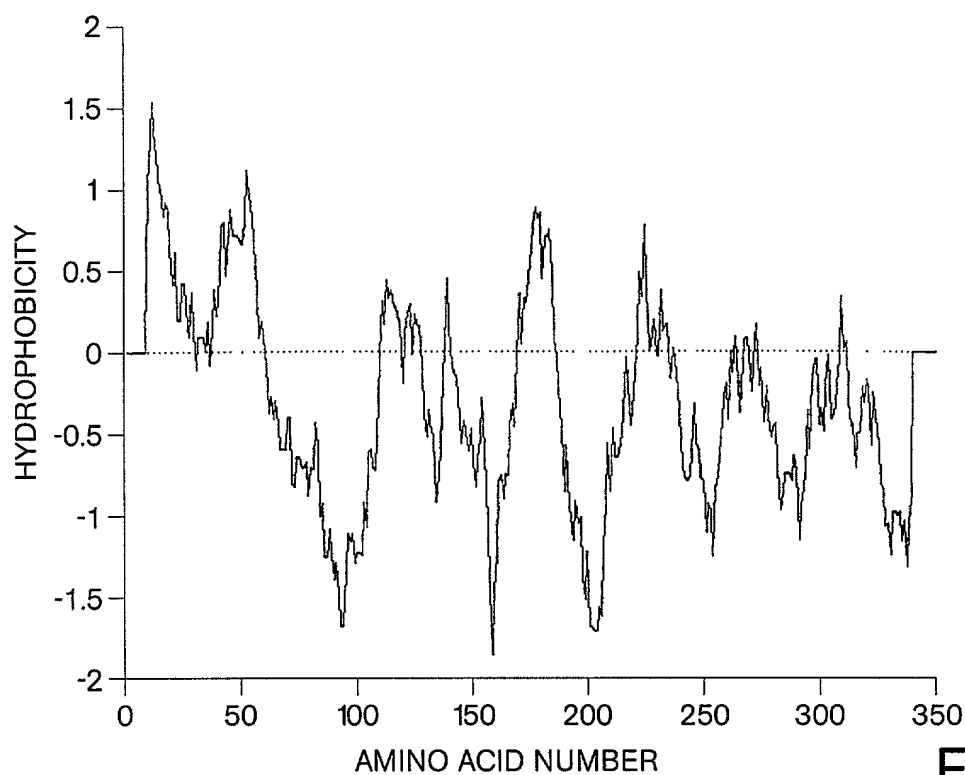


Fig. 18

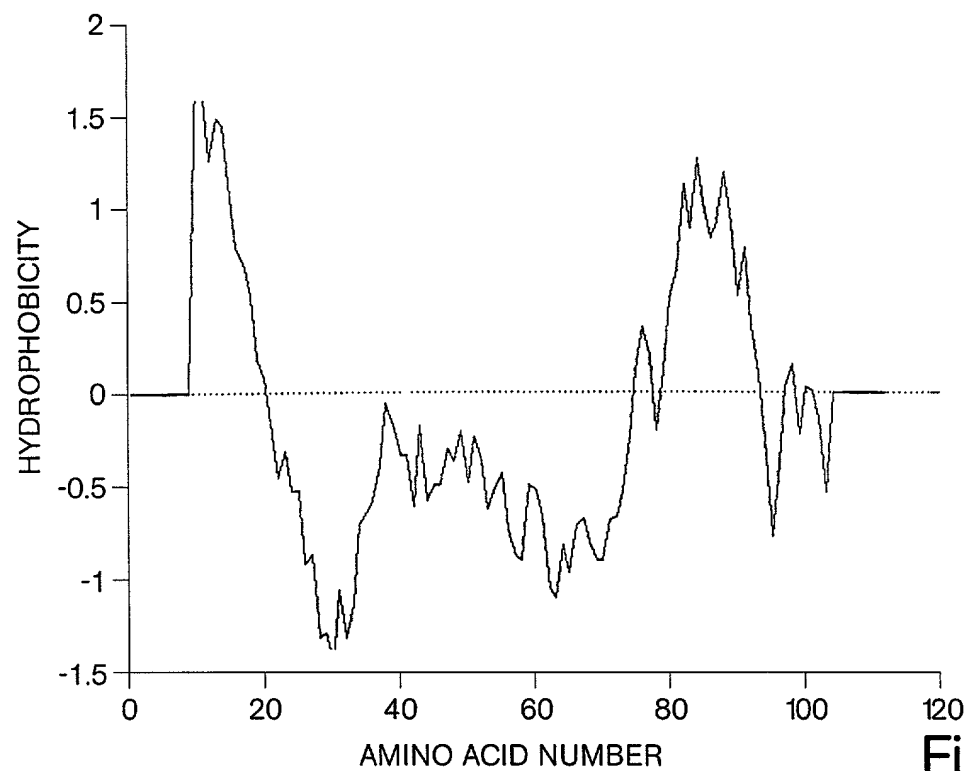


Fig. 19

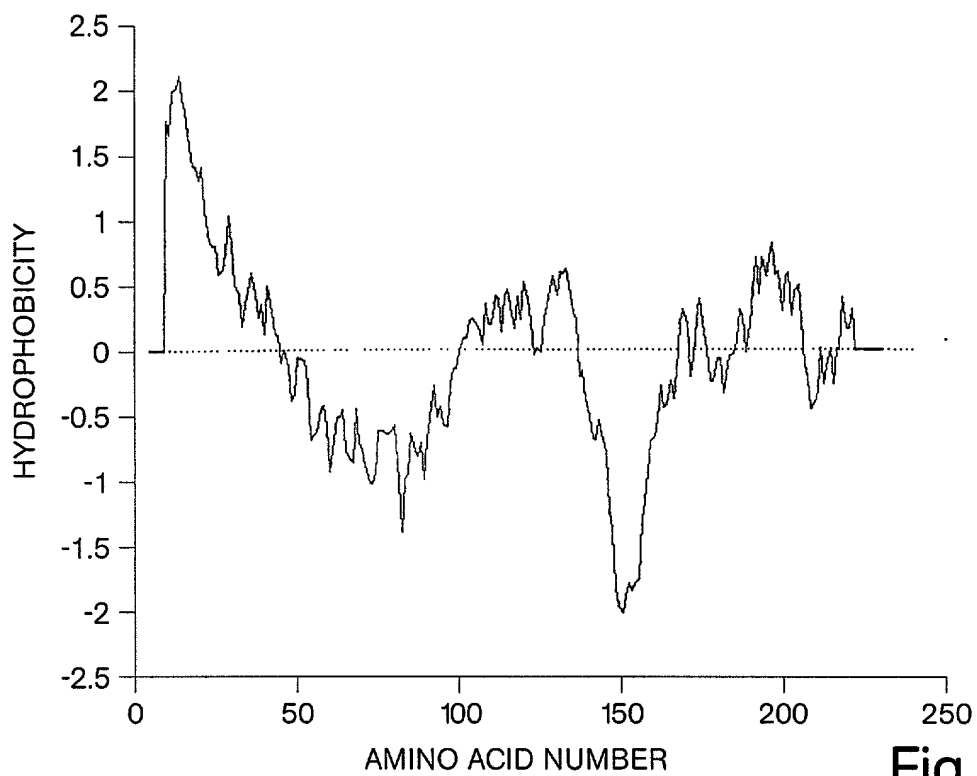


Fig. 20

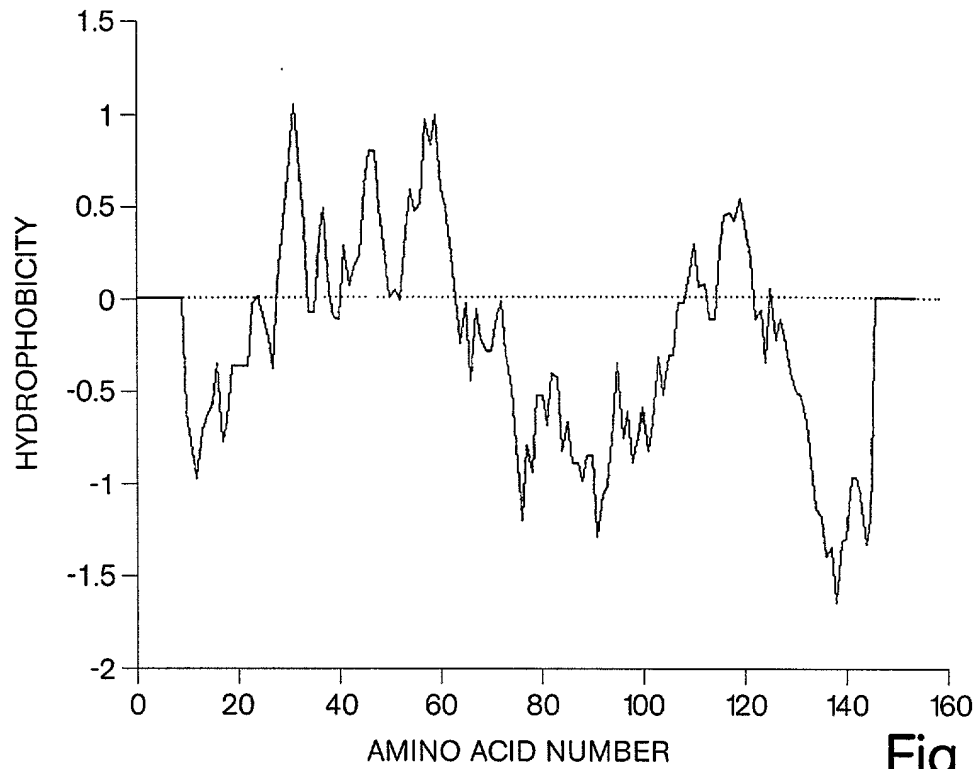


Fig. 21

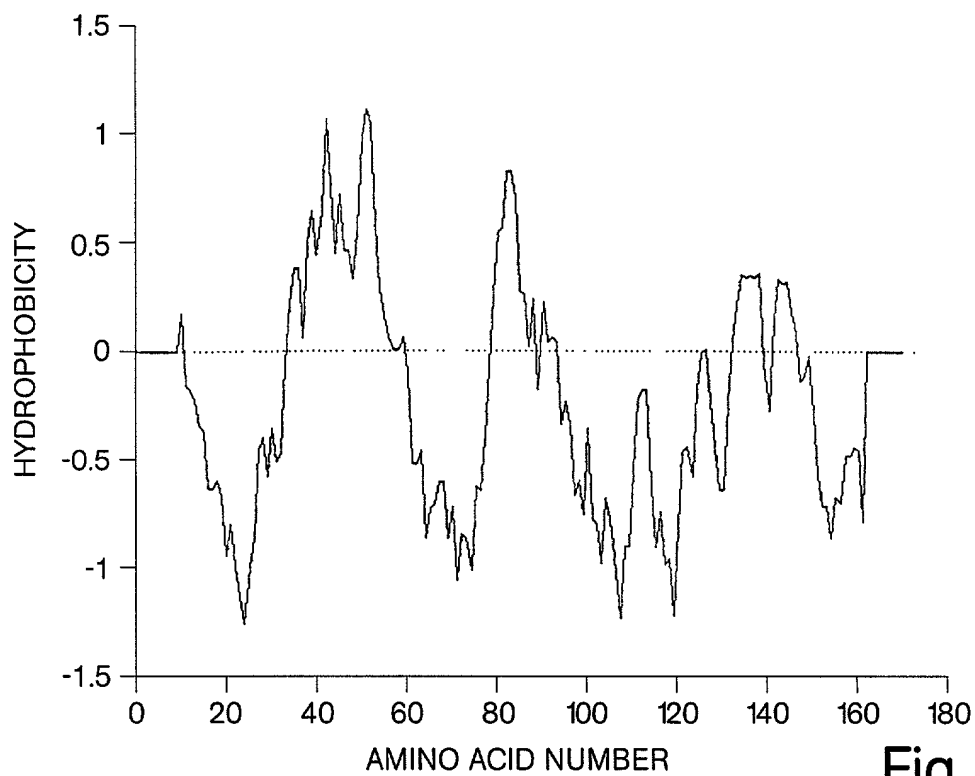


Fig. 22

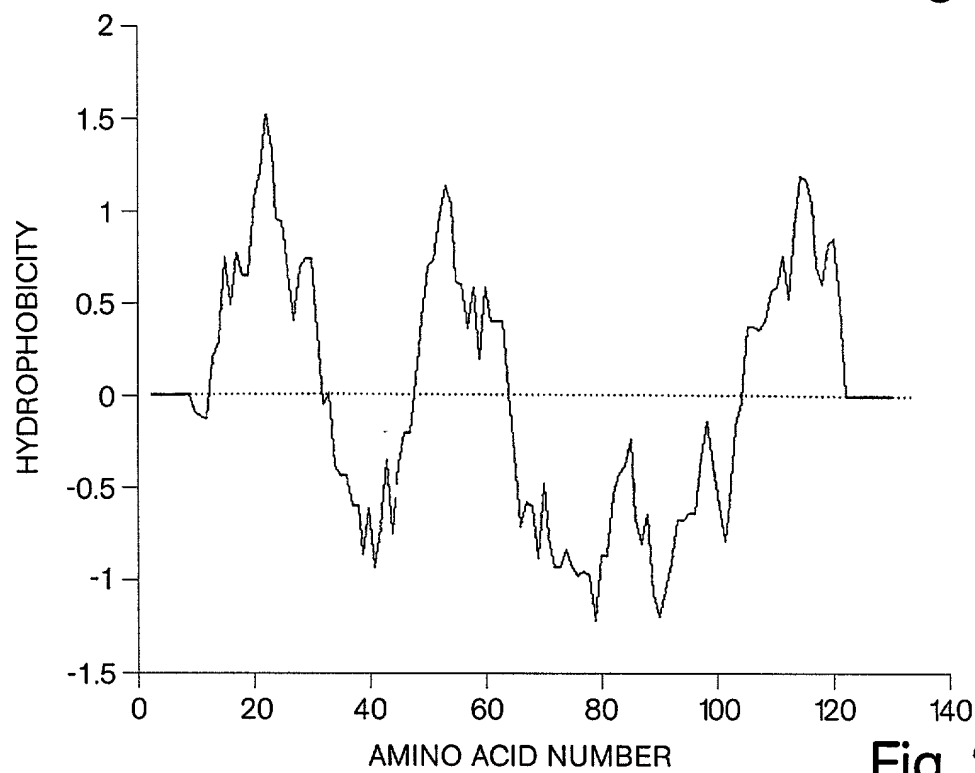


Fig. 23